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MOLECULAR TRACING OF VIRAL PATHOGENS IN AQUACULTURE -A MULTIDISCIPLINARY TRANS-EUROPEAN RESEARCH PROJECT

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INTRODUCTION

Viral diseases threaten sustainable aquaculture production of both fish and molluscs worldwide. In Europe, the most important viral diseases include infection with viruses in the families Alphaviridae, Rhabdoviridae, Betanodaviridae, Malaco- and Alloherpesviridae. Considerable resources are invested in controlling the spread of viral pathogens in aquaculture. Control strategies have generally been designed based on general knowledge on biosecurity and only to a very limited degree take into account disease-specific transmission patterns. This leads to compromised efficiency of preventive interventions. New EU-legislation requires that surveillance of aquaculture diseases be risk-based, but knowledge on risks and their prevention is poor.

Here we present a new research-project funded under the EMIDA-ERA Net under the EU 7th Framework program.

PROJECT AIMS

Assemble spatio-temporal epidemiological data for important host-pathogen systems to identify important factors affecting the spread of diseases

Gain knowledge into the factors that control viral spread at the molecular level

Assess effects of various control strategies for selected host-pathogen systems

SPECIFIC OBJECTIVES

- Collection of isolates of specific important aquatic animal viruses and their respective epidemiological data
- Caracterisation of the isolates by phylogenetic and expression analyses
- Constructing scenario simulation models to assess effects of different control strategies.

EXPECTED OUTCOMES

- Increased knowledge on virus diversity, distribution and partly pathogenesis, and on factors affecting the spread of disease in aquaculture including virus release into the environment.
- Identification of possible virulence markers, and identity between viruses and their molecular characterization.
- Scenario simulation models to assess effects of various control strategies will be designed and used, which can then be formulated as recommendations for cost-effective control of diseases in aquaculture.

PROJECT PARTNERS

Veterinærinstituttet – Norwegian Veterinary Institute

Ifremer

Technical University of Denmark – National Veterinary Institute – DTU

anses – alimentation, environnement, travail

NR Norsk Regnesentral – Norwegian Computing Center

Friedrich-Loeffler-Institut – FLI – Bundesforschungsinstitut für Tiergesundheit – Federal Research Institute for Animal Health

IRD – Institut de recherche pour le développement

PROJECT PLAN

WP 1: Project co-ordination and consortium management.
This WP coordinates and manages all aspects regarding the administration of the project. All legal, contractual, ethical, financial and administrative management of the project and all communication with the EMIDA CO are taken care of in this WP.

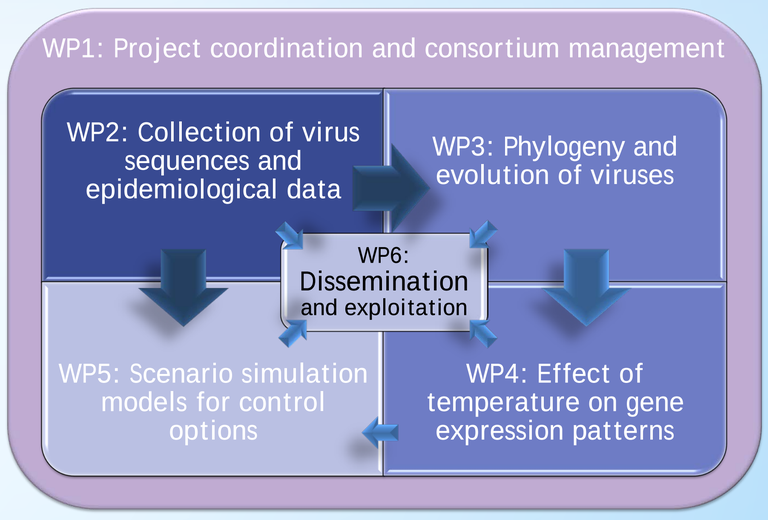
WP 2: Collection of virus sequences and epidemiological data.
The aim of WP2 is to provide high quality data on samples of representative isolates belonging to various fish and shellfish viruses including part- and whole genome sequences together with epidemiological data. The genetic diversity of all viruses in this joint collection are investigated based on classic PCR-sequencing of specific regions of the viral genome from virus isolates and biological samples. The epidemiological data on isolates of the viruses included in the project are collated and systematized and uploaded in the isolate database http://www.fishpathogens.eu

WP 3: Phylogeny and evolution of viruses.
WP3 has three goals:
Identifying and classifying each viral isolate among its related species
Selecting genotypes of particular interest for gene expression studies in WP4
Shedding light on the mechanisms of variations and evolution of viral populations.
The sequences furnished by partners will be assembled in phylogenetic trees with methods specific of each viral family. Genetic regions showing the highest variations will be listed and hypotheses on their relation to virulence and geographical origins emitted.

WP 4: Investigation of the effect of temperature on gene expression patterns.
This WP will gain knowledge into the factors that control viral spread at the molecular level. The effect of temperature on viral gene expression will be investigated, as temperature plays a key role in triggering virulence of almost all fish viruses.
Oligonucleotide microarrays will be designed to cover both the full transcriptome of the large DNA viruses and the entire diversity of the small RNA viruses. The large collections of viruses available within the consortium allows for investigation of isolates that display varying genotypes, comparing strains with different phenotypes (i.e. virulent vs avirulent strains).

WP 5: Scenario simulation models for control options.
WP 5 is dedicated to developing generic modelling tools for exploring effects of different intervention strategies on the incidence of disease outbreaks in aquaculture. The models will be used to investigate different intervention strategies to reduce the number of disease outbreaks in the future, using numeric simulations of disease spread under various scenarios. Interventions such as progressed culling of infected farm stocks, neighbourhood surveillance and culling, or vaccination, are topics that will be explored.

WP 6: Dissemination and exploitation.
WP6 deals with the dissemination and exploitation of the project findings to the public, the scientific community and the stakeholders. This will be done mainly as presentations at international scientific conferences, workshops and as publications in scientific peer-reviewed journals.



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